

(1) GENERAL INFORMATION

(i) APPLICANT: Lal, Preeti
Hillman, Jennifer
Corley, Neil
Shah, Purvi

(ii) TITLE OF THE INVENTION: HUMAN PHOSPHOLIPID BINDING PROTEINS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

(B) STREET: 3174 Porter Dr.

(C) CITY: Palo Alto

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned

(B) FILING DATE: Filed Herewith

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.

(B) REGISTRATION NUMBER: 36,749

(C) REFERENCE/DOCKET NUMBER: PF-0379 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555

(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: MUSCNOT07

(B) CLONE: 3014759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Ala Ala Gly Ser Phe Ser Glu Glu Gln Phe Trp Glu Ala
1 5 10 15
Cys Ala Glu Leu Gln Gln Pro Ala Leu Ala Gly Ala Asp Trp Gln Leu

	20		25		30										
Leu	Val	Glu	Thr	Ser	Gly	Ile	Ser	Ile	Tyr	Arg	Leu	Leu	Asp	Lys	Lys
	35						40					45			
Thr	Gly	Leu	Tyr	Glu	Tyr	Lys	Val	Phe	Gly	Val	Leu	Glu	Asp	Cys	Ser
	50					55					60				
Pro	Thr	Leu	Leu	Ala	Asp	Ile	Tyr	Met	Asp	Ser	Asp	Tyr	Arg	Lys	Gln
65					70				75					80	
Trp	Asp	Gln	Tyr	Val	Lys	Glu	Leu	Tyr	Glu	Gln	Glu	Cys	Asn	Gly	Glu
				85					90					95	
Thr	Val	Val	Tyr	Trp	Glu	Val	Lys	Tyr	Pro	Phe	Pro	Met	Ser	Asn	Arg
			100					105					110		
Asp	Tyr	Val	Tyr	Leu	Arg	Gln	Arg	Arg	Asp	Leu	Asp	Met	Glu	Gly	Arg
		115					120					125			
Lys	Ile	His	Val	Ile	Leu	Ala	Arg	Ser	Thr	Ser	Met	Pro	Gln	Leu	Gly
	130					135					140				
Glu	Arg	Ser	Gly	Val	Ile	Arg	Val	Lys	Gln	Tyr	Lys	Gln	Ser	Leu	Ala
145					150					155					160
Ile	Glu	Ser	Asp	Gly	Lys	Lys	Gly	Ser	Lys	Val	Phe	Met	Tyr	Tyr	Phe
				165					170					175	
Asp	Asn	Pro	Gly	Gly	Gln	Ile	Pro	Ser	Trp	Leu	Ile	Asn	Trp	Ala	Ala
			180					185					190		
Lys	Asn	Gly	Val	Pro	Asn	Phe	Leu	Lys	Asp	Met	Ala	Arg	Ala	Cys	Gln
		195					200					205			
Asn	Tyr	Leu	Lys	Lys	Thr										
	210														

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2051 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MUSCNOT07
 (B) CLONE: 3014759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCAGTTTCCT	GCCAATGACG	CTGGGGCAGC	CGGGGCAGCC	GGGGCAGCCC	GGTCACCCCG	60
CCCCCAGGCC	CACACTAAGG	GTGTCCGCGG	CCTGCCCTCC	AGGCGGAGGA	GCCCGGACTG	120
CGGAAGGATG	GAGCTGGCCG	CCGGAAGCTT	CTCGGAGGAG	CAGTTCTGGG	AGGCCTGCGC	180
CGAGCTCCAG	CAGCCCGCTC	TGGCCGGGGC	CGACTGGCAG	CTCCTAGTGG	AGACCTCGGG	240
CATCAGCATC	TACCGGCTGC	TGGACAAGAA	GACTGGACTT	TATGAGTATA	AAGTCTTTGG	300
TGTTCTGGAG	GACTGCTCAC	CAACTCTACT	GGCAGACATC	TATATGGACT	CAGATTACAG	360
AAAACAATGG	GACCAGTATG	TTAAAGAACT	CTATGAACAA	GAATGCAACG	GAGAGACTGT	420
GGTCTACTGG	GAAGTGAAGT	ACCCTTTTCC	CATGTCCAAC	AGAGACTATG	TCTACCTTCG	480
GCAGCGGCGA	GACCTGGACA	TGGAAGGGAG	GAAGATCCAT	GTGATCCTGG	CCCGGAGCAC	540
CTCCATGCCT	CAGCTTGGCG	AGAGGTCTGG	GGTGATCCGG	GTGAAGCAAT	ACAAGCAGAG	600
CCTGGCGATT	GAGAGTGACG	GCAAGAAGGG	GAGCAAAGTT	TTCATGTATT	ACTTCGATAA	660
3 CCCGGGTGGC	CAAATTCCGT	CCTGGCTCAT	TAAGTGGGCC	GCCAAGAATG	GAGTTCCTAA	720
CTTCTTGAAA	GACATGGCAA	GAGCCTGTCA	GAAGTACCTC	AAGAAAACCT	AAGAAAGAGA	780
ACTGGGAACA	TTGCATCCAT	GGGTTGATGT	CTCTGGAAGT	GCAACCACCC	AATGTCTCTG	840
GAAGTGCCAC	CTGGAAGTGC	CACCTGGAAG	TGTCTCTGGA	AGAGCACCCA	CCACTGTTCA	900
GCCTTCCCCCT	GCTGPTTCTG	TCTTCAGAGG	CCTACACACT	ACCACATCCT	TTCTAAGCAT	960
GTTTGCCTGA	CATCCAGCTC	ACTCGTCTGC	TTCCTTTCTC	GCTCCCCCCC	ATCCTGGGGC	1020
TGGGGCTGCC	TTCTTCTACA	GTTCAATATG	GGGCAGACTA	GGGAAACCTT	TGCTTGCTTA	1080
CTATTAGGAG	GGGAAGTCTT	CAGTAGGGAA	CACGATCATT	CCATTGTGCA	ATTTTACGGG	1140
GATGGGTGGG	CGGAGGGACA	CAACAAAATT	TAAGAATGAC	TATTTGGGCG	GGCTGGCTCT	1200
TTTGCAGCTT	GTGATTTCTT	CCAGCTTGGG	AGGGGCTGCT	GGAAGTGGCA	TTTCGTTTCA	1260
AGCTGACTTT	CAGTGCACCC	AAACTGGATG	ACGTGCCAAT	GTCCATTTGC	CTTATGCTTT	1320
GTGGAGCTGA	TTAGGCTGGG	ATTTGAGGTG	ATAATCCAGT	AAGTCTTTCC	TCGTTCCTAC	1380
TTGTGGAGGA	TCAGTAGCTG	TTATGATGCC	AGACCATTTG	GAGAAGTATC	AGAGGCCTGA	1440
CCGGACACAT	AATACGACAA	CCACATTTT	CCTCATCATC	CATGAGGAAA	TGGATGATTT	1500
CTCTTTTCCA	TATGTCACTG	GGGGAAAGGC	TGCCTGTACC	TCTCAAGCTT	TGCATTTTAC	1560

TGGAAACTGA	GCGTCAAGA	TGGCTGTGGC	CAGCTAGCAA	AAGCAAAGAT	GCTTTGTGCA	1620
TAGCCTTGTG	AAAAAGTATC	TTTCTATGCA	ATAAGATGAA	TTTTCCTCCC	AGAATATTTA	1680
GAAATGTAGA	AGGGATAACA	GTTACACAGCC	AGGTAAAATT	TAAGTGGTGG	CTTAATGACT	1740
CTGCACCTTT	TTCTCAGGAA	TTCTGCCTAA	GTTGTCTGCC	TTTTCTACCA	CCAAAAAGAC	1800
TTTGTAGTTT	CTATGCTTTC	TCCTGAATTT	TGGTAGGGTA	AGGTATTTCT	ATGTCAAAGG	1860
CACAGCCTTG	ATGATCTCAG	GGAAAAATTT	TAATCACTGT	GTATAATGAT	ACTGAACCTT	1920
GATTAATAAC	AGAAATTCAG	GATGTAAAGC	CACAGAATGG	GATTTATTAA	TGTGGGATAC	1980
CTCAGACTGT	TTGTTTTCTT	TCTGGGAAGA	AAAGTGTGTT	CTATAATGAA	TAAATATAGA	2040
GTGGTTTTTA	A					2051

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT12
- (B) CLONE: 3126479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
1 5 10 15
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
20 25 30
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
35 40 45
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
50 55 60
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
65 70 75 80
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
85 90 95
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
100 105 110
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Glu Gly Lys Ile
115 120 125
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
130 135 140
Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
145 150 155 160
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
165 170 175
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
180 185 190
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
195 200 205
Pro Arg Gly Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
210 215 220
Ala Ala Cys
225

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGTUT12

(B) CLONE: 3126479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGTACTTGTG	TCCGGGTGGT	GGACTGGATT	CGCTGCGGAG	CCCTGGAAGC	TGCCTTTCCT	60
TCTCCCTGTG	CTTAACCAGA	GGTGCCCATG	GGTTGGACAA	TGAGGCTGGT	CACAGCAGCA	120
CTGTTACTGG	GTCTCATGAT	GGTGGTCACT	GGAGACGAGG	ATGAGAACAG	CCCGTGTGCC	180
CATGAGGCCC	TCTTGGACGA	GGACACCCTC	TTTTGCCAGG	GCCTTGAAGT	TTTCTACCCA	240
GAGTTGGGGA	ACATTGGCTG	CAAGGTTGTT	CCTGATTGTA	ACAACCTACAG	ACAGAAGATC	300
ACCTCCTGGA	TGGAGCCGAT	AGTCAAGTTC	CCGGGGGCCG	TGGACGGCGC	AACCTATATC	360
CTGGTGATGG	TGGATCCAGA	TGCCCCTAGC	AGAGCAGAAC	CCAGACAGAG	ATTCTGGAGA	420
CATTGGCTGG	TAACAGATAT	CAAGGGCGCC	GACCTGAAGG	AAGGGAAGAT	TCAGGGCCAG	480
GAGTTATCAG	CCTACCAGGC	TCCCTCCCCA	CCGGCACACA	GTGGCTTCCA	TCGCTACCAG	540
TTCTTTGTCT	ATCTTCAGGA	AGGAAAAGTC	ATCTCTCTCC	TTCCCAAGGA	AAACAAAACCT	600
CGAGGCTCTT	GGAAAATGGA	CAGATTTCTG	AACCGCTTCC	ACCTGGGCGA	ACCTGAAGCA	660
AGCACCCAGT	TCATGACCCA	GAACCTACCAG	GACTCACCAA	CCCTCCAGGC	TCCCAGAGGA	720
AGGGCCAGCG	AGCCCAAGCA	CAAAAACCAG	GCGGAGATAG	CTGCCTGCTA	GATAGCCGGC	780
TTTGCCATCC	GGGCATGTGG	CCACACTGCC	CACCACCGAC	GATGTGGGTA	TGGAACCCCC	840
TCTGGATACA	GAACCCCTTC	TTTTCCAAAT	AAAAAAAAAA	TCATCCAGGG	CTTGGTGCTT	900
TGT						903

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 897693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asp	Pro	Gly	Ala	Gly	Ala	Phe	Ser	Glu	Glu	Gln	Phe	Arg	Glu	Ala
1				5					10					15	
Cys	Ala	Glu	Leu	Gln	Arg	Pro	Ala	Leu	Ser	Gly	Ala	Ala	Trp	Glu	Leu
			20					25					30		
Leu	Val	Glu	Thr	Gln	Gly	Ile	Ser	Val	Tyr	Arg	Leu	Leu	Asp	Gln	Gln
			35				40					45			
Thr	Gly	Leu	Tyr	Ala	Tyr	Lys	Val	Phe	Gly	Val	Leu	Glu	Asp	Cys	Leu
			50			55					60				
Pro	Asp	Leu	Leu	Ala	Asp	Val	Tyr	Met	Asp	Leu	Ala	Tyr	Arg	Lys	Gln
65				70					75					80	
Trp	Asp	Gln	Tyr	Val	Lys	Glu	Leu	Tyr	Glu	Lys	Glu	Cys	Ser	Gly	Glu
				85				90					95		
Thr	Val	Val	Tyr	Trp	Gln	Val	Lys	Tyr	Pro	Phe	Pro	Met	Ser	Asn	Arg
			100					105					110		
Asp	Tyr	Val	Tyr	Val	Arg	Gln	Arg	Gln	Glu	Leu	Asp	Phe	Glu	Gly	Gln
			115			120						125			
Lys	Val	His	Val	Ile	Leu	Ala	Gln	Ser	Thr	Ser	Glu	Pro	Gln	Phe	Pro
			130			135					140				
Glu	Lys	Ser	Gly	Val	Ile	Arg	Val	Lys	His	Tyr	Lys	Gln	Arg	Leu	Ala
145				150					155					160	
Ile	Gln	Ser	Asp	Gly	Lys	Lys	Gly	Ser	Lys	Val	Phe	Met	Tyr	Tyr	Phe
			165					170					175		
Asp	Asn	Pro	Gly	Gly	Gln	Ile	Pro	Ser	Trp	Val	Ile	Asn	Trp	Ala	Ala
			180					185					190		
Lys	Asn	Gly	Val	Pro	Asn	Phe	Leu	Lys	Asp	Met	Val	Lys	Ala	Cys	Gln
			195				200					205			
Asn	Tyr	Lys	Lys	Thr											
			210												

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1143527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val	Val	Ser	Thr	Ser	Pro	Thr	Lys	Leu	Val	Asn	Val	Ser	Tyr	Asn	Asn
1				5					10					15	
Leu	Thr	Val	Asn	Leu	Gly	Asn	Glu	Leu	Thr	Pro	Thr	Gln	Val	Lys	Asn
			20					25					30		
Gln	Pro	Thr	Lys	Val	Ser	Trp	Asp	Ala	Glu	Pro	Gly	Ala	Leu	Tyr	Thr
		35				40						45			
Leu	Val	Met	Thr	Asp	Pro	Asp	Ala	Pro	Ser	Arg	Lys	Asn	Pro	Val	Phe
	50					55					60				
Arg	Glu	Trp	His	His	Trp	Leu	Ile	Ile	Asn	Ile	Ser	Gly	Gln	Asn	Val
65					70					75				80	
Ser	Ser	Gly	Thr	Val	Leu	Ser	Asp	Tyr	Ile	Gly	Ser	Gly	Pro	Pro	Lys
			85						90				95		
Gly	Thr	Gly	Leu	His	Arg	Tyr	Val	Phe	Leu	Val	Tyr	Lys	Gln	Pro	Gly
			100					105					110		
Ser	Ile	Thr	Asp	Thr	Gln	His	Gly	Gly	Asn	Arg	Pro	Asn	Phe	Lys	Val
		115					120					125			
Met	Asp	Phe	Ala	Asn	Lys	His	His	Leu	Gly	Asn	Pro	Val	Ala	Gly	Asn
	130					135					140				
Phe	Phe	Gln	Ala	Lys	His	Glu	Asp								
145					150										

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